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RAW SEQUENCE LISTING                     DATE: 08/07/2002
PATENT APPLICATION:  US/09/542,520B      TIME: 15:57:24

         Input Set : A:\EP.txt
         Output Set: N:\CRF3\08072002\I542520B.raw
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 5 <110> APPLICANT: Jackson, W. James
 6        Pace, John
 8 <120> TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
10 <130> FILE REFERENCE: 7969-076-999
12 <140> CURRENT APPLICATION NUMBER: 09/542,520B
13 <141> CURRENT FILING DATE: 2000-04-03
15 <150> PRIOR APPLICATION NUMBER: 08/942,596
16 <151> PRIOR FILING DATE: 1997-10-02
18 <160> NUMBER OF SEQ ID NOS: 43
20 <170> SOFTWARE: PatentIn version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 4435
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Description of Artificial Sequence: Recombinant Expression
Vector
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (382)..(3417)
33 <223> OTHER INFORMATION:
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37 gcgccacggg ttttggggcg gaatgaattt tttcgttccg gaaaaagtaa ttccccggga     120
38 acgtagggta tcggtttcat aggctcgcca aatgggatat aggtggaaag gtaaaaaaaa     180
39 ctgagccaag caaaggatag agaagtcttg taatcatcgc aggttaaagg ggggatgtta     240
40 ttttagcctg caaatagtgt aattattgga tcctgtaaag agaaaaggac gaatgcgctg     300
41 aagataagaa catttattga tattaaatta ttaatttttt atgaagcgga gtaattaatt     360
42 ttatctctca gctttttgtgt g atg caa acg tct ttc cat aag ttc ttt ctt     411
43                           Met Gln Thr Ser Phe His Lys Phe Phe Leu
44                            1               5                  10
45 tca atg att cta gct tat tct tgc tgc tct tta aat ggg ggg gga tat     459
47 Ser Met Ile Leu Ala Tyr Ser Cys Cys Ser Leu Asn Gly Gly Gly Tyr
48                  15                  20                  25
49 gca gca gaa atc atg gtt cct caa gga att tac gat ggg gag acg tta     507
50 Ala Ala Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu
51                  30                  35                  40
52 act gta tca ttt ccc tat act gtt ata gga gat ccg agt ggg act act     555
53 Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr
54          45                  50                  55
55 gtt ttt tct gca gga gag tta aca tta aaa aat ctt gac aat tct att     603
56 Val Phe Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile
57      60                  65                  70
58 gca gct ttg cct tta agt tgt ttt ggg aac tta tta ggg agt ttt act     651
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59 Ala Ala Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr
60 75                  80                  85                  90
61 gtt tta ggg aga gga cac tcg ttg act ttc gag aac ata cgg act tct        699
62 Val Leu Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser
63                  95                  100                 105
64 aca aat ggg gca gct cta agt aat agc gct gct gat gga ctg ttt act        747
65 Thr Asn Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr
66                 110                 115                 120
67 att gag ggt ttt aaa gaa tta tcc ttt tcc aat tgc aat tca tta ctt        795
68 Ile Glu Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu
69             125                 130                 135
70 gcc gta ctg cct gct gca acg act aat aag ggt agc cag act ccg acg        843
71 Ala Val Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr
72         140                 145                 150
73 aca aca tct aca ccg tct aat ggt act att tat tct aaa aca gat ctt        891
74 Thr Thr Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu
75 155                 160                 165                 170
76 ttg tta ctc aat aat gag aag ttc tca ttc tat agt aat tta gtc tct        939
77 Leu Leu Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser
78                 175                 180                 185
79 gga gat ggg gga gct ata gat gct aag agc tta acg gtt caa gga att        987
80 Gly Asp Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile
81             190                 195                 200
82 agc aag ctt tgt gtc ttc caa gaa aat act gct caa gct gat ggg gga       1035
83 Ser Lys Leu Cys Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly
84         205                 210                 215
85 gct tgt caa gta gtc acc agt ttc tct gct atg gct aac gag gct cct       1083
86 Ala Cys Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro
87     220                 225                 230
88 att gcc ttt gta gcg aat gtt gca gga gta aga ggg gga ggg att gct       1131
89 Ile Ala Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly Ile Ala
90 235                 240                 245                 250
91 gct gtt cag gat ggg cag cag gga gtg tca tca tct act tca aca gaa       1179
93 Ala Val Gln Asp Gly Gln Gln Gly Val Ser Ser Ser Thr Ser Thr Glu
94                 255                 260                 265
95 gat cca gta gta agt ttt tcc aga aat act gcg gta gag ttt gat ggg       1227
96 Asp Pro Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly
97             270                 275                 280
98 aac gta gcc cga gta gga gga ggg att tac tcc tac ggg aac gtt gct       1275
99 Asn Val Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala
100         285                 290                 295
101 ttc ctg aat aat gga aaa acc ttg ttt ctc aac aat gtt gct tct cct      1323
102 Phe Leu Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro
103         300                 305                 310
104 gtt tac att gct gct aag caa cca aca agt gga cag gct tct aat acg      1371
105 Val Tyr Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr
106 315                 320                 325                 330
107 agt aat aat tac gga gat gga gga gct atc ttc tgt aag aat ggt gcg      1419
108 Ser Asn Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala
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109                335                340                345
110 caa gca gga tcc aat aac tct gga tca gtt tcc ttt gat gga gag gga    1467
111 Gln Ala Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly
112                350                355                360
113 gta gtt ttc ttt agt agc aat gta gct gct ggg aaa ggg gga gct att    1515
114 Val Val Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile
115                365                370                375
116 tat gcc aaa aag ctc tcg gtt gct aac tgt ggc cct gta caa ttt tta    1563
117 Tyr Ala Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu
118     380                385                390
119 agg aat atc gct aat gat ggt gga gcg att tat tta gga gaa tct gga    1611
120 Arg Asn Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly
121 395                400                405                410
122 gag ctc agt tta tct gct gat tat gga gat att att ttc gat ggg aat    1659
123 Glu Leu Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn
124                415                420                425
130 ctt aaa aga aca gcc aaa gag aat gct gcc gat gtt aat ggc gta act    1707
131 Leu Lys Arg Thr Ala Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr
132                430                435                440
133 gtg tcc tca caa gcc att tcg atg gga tcg gga ggg aaa ata acg aca    1755
134 Val Ser Ser Gln Ala Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr
135                445                450                455
136 tta aga gct aaa gca ggg cat cag att ctc ttt aat gat ccc atc gag    1803
137 Leu Arg Ala Lys Ala Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu
139     460                465                470
140 atg gca aac gga aat aac cag cca gcg cag tct tcc aaa ctt cta aaa    1851
141 Met Ala Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys
142 475                480                485                490
143 att aac gat ggt gaa gga tac aca ggg gat att gtt ttt gct aat gga    1899
144 Ile Asn Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly
145                495                500                505
146 agc agt act ttg tac caa aat gtt acg ata gag caa gga agg att gtt    1947
147 Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val
148                510                515                520
149 ctt cgt gaa aag gca aaa tta tca gtg aat tct cta agt cag aca ggt    1995
150 Leu Arg Glu Lys Ala Lys Leu Ser Val Asn Ser Leu Ser Gln Thr Gly
151                525                530                535
152 ggg agt ctg tat atg gaa gct ggg agt aca tgg gat ttt gta act cca    2043
153 Gly Ser Leu Tyr Met Glu Ala Gly Ser Thr Trp Asp Phe Val Thr Pro
154     540                545                550
155 caa cca cca caa cag cct cct gcc gct aat cag ttg atc acg ctt tcc    2091
156 Gln Pro Pro Gln Gln Pro Pro Ala Ala Asn Gln Leu Ile Thr Leu Ser
157 555                560                565                570
158 aat ctg cat ttg tct ctt tct tct ttg tta gca aac aat gca gtt acg    2139
159 Asn Leu His Leu Ser Leu Ser Ser Leu Leu Ala Asn Asn Ala Val Thr
160                575                580                585
161 aat cct cct acc aat cct cca gcg caa gat tct cat cct gca gtc att    2187
162 Asn Pro Pro Thr Asn Pro Pro Ala Gln Asp Ser His Pro Ala Val Ile
163                590                595                600
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164 ggt agc aca act gct ggt tct gtt aca att agt ggg cct atc ttt ttt    2235
165 Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile Phe Phe
166         605                 610                 615
167 gag gat ttg gat gat aca gct tat gat agg tat gat tgg cta ggt tct    2283
168 Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu Gly Ser
169     620                 625                 630
170 aat caa aaa atc aat gtc ctg aaa tta cag tta ggg act aag ccc cca    2331
171 Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu Gly Thr Lys Pro Pro
172 635                 640                 645                 650
173 gct aat gcc cca tca gat ttg act cta ggg aat gag atg cct aag tat    2379
174 Ala Asn Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu Met Pro Lys Tyr
175                 655                 660                 665
176 ggc tat caa gga agc tgg aag ctt gcg tgg gat cct aat aca gca aat    2427
177 Gly Tyr Gln Gly Ser Trp Lys Leu Ala Trp Asp Pro Asn Thr Ala Asn
178                 670                 675                 680
179 aat ggt cct tat act ctg aaa gct aca tgg act aaa act ggg tat aat    2475
180 Asn Gly Pro Tyr Thr Leu Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn
181                 685                 690                 695
182 cct ggg cct gag cga gta gct tct ttg gtt cca aat agt tta tgg gga    2523
183 Pro Gly Pro Glu Arg Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly
185         700                 705                 710
186 tcc att tta gat ata cga tct gcg cat tca gca att caa gca agt gtg    2571
187 Ser Ile Leu Asp Ile Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val
188 715                 720                 725                 730
189 gat ggg cgc tct tat tgt cga gga tta tgg gtt tct gga gtt tcg aat    2619
190 Asp Gly Arg Ser Tyr Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn
191                 735                 740                 745
192 ttc ttc tat cat gac cgc gat gct tta ggt cag gga tat cgg tat att    2667
193 Phe Phe Tyr His Asp Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile
194                 750                 755                 760
195 agt ggg ggt tat tcc tta gga gca aac tcc tac ttt gga tca tcg atg    2715
196 Ser Gly Gly Tyr Ser Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met
197         765                 770                 775
198 ttt ggt cta gca ttt acc gaa gta ttt ggt aga tct aaa gat tat gta    2763
199 Phe Gly Leu Ala Phe Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val
200     780                 785                 790
201 gtg tgt cgt tcc aat cat cat gct tgc ata gga tcc gtt tat cta tct    2811
202 Val Cys Arg Ser Asn His His Ala Cys Ile Gly Ser Val Tyr Leu Ser
203 795                 800                 805                 810
204 acc caa caa gct tta tgt gga tcc tat ttg ttc gga gat gcg ttt atc    2859
205 Thr Gln Gln Ala Leu Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile
206                 815                 820                 825
207 cgt gct agc tac ggg ttt ggg aat cag cat atg aaa acc tca tat aca    2907
208 Arg Ala Ser Tyr Gly Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr
209                 830                 835                 840
210 ttt gca gag gag agc gat gtt cgt tgg gat aat aac tgt ctg gct gga    2955
211 Phe Ala Glu Glu Ser Asp Val Arg Trp Asp Asn Asn Cys Leu Ala Gly
212                 845                 850                 855
213 gag att gga gcg gga tta ccg att gtg att act cca tct aag ctc tat    3003
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Input Set : A:\EP.txt
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214 Glu Ile Gly Ala Gly Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr
215     860                 865             870
216 ttg aat gag ttg cgt cct ttc gtg caa gct gag ttt tct tat gcc gat      3051
217 Leu Asn Glu Leu Arg Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp
218 875                 880             885                 890
219 cat gaa tct ttt aca gag gaa ggc gat caa gct cgg gca ttc aag agc      3099
220 His Glu Ser Phe Thr Glu Glu Gly Asp Gln Ala Arg Ala Phe Lys Ser
221             895                 900             905
222 gga cat ctc cta aat cta tca gtt cct gtt gga gtg aag ttt gat cga      3147
223 Gly His Leu Leu Asn Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg
224             910                 915             920
225 tgt tct agt aca cat cct aat aaa tat agc ttt atg gcg gct tat atc      3195
226 Cys Ser Ser Thr His Pro Asn Lys Tyr Ser Phe Met Ala Ala Tyr Ile
227         925             930             935
228 tgt gat gct tat cgc acc atc tct ggt act gag aca acg ctc cta tcc      3243
229 Cys Asp Ala Tyr Arg Thr Ile Ser Gly Thr Glu Thr Thr Leu Leu Ser
231     940             945             950
232 cat caa gag aca tgg aca aca gat gcc ttt cat tta gca aga cat gga      3291
233 His Gln Glu Thr Trp Thr Thr Asp Ala Phe His Leu Ala Arg His Gly
234 955                 960             965                 970
235 gtt gtg gtt aga gga tct atg tat gct tct cta aca agt aat ata gaa      3339
236 Val Val Val Arg Gly Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu
237             975             980             985
238 gta tat ggc cat gga aga tat gag tat cga gat gct tct cga  ggc tat     3387
239 Val Tyr Gly His Gly Arg Tyr Glu Tyr Arg Asp Ala Ser Arg  Gly Tyr
240             990             995             1000
241 ggt ttg agt  gca gga agt aga gtc  cgg ttc taaaaatatt ggttagatag      3437
242 Gly Leu Ser  Ala Gly Ser Arg Val  Arg Phe
243         1005             1010
244 ttaagtgtta gcgatgcctt tttctttgag atctacatca ttttgttttt tagcttgttt    3497
245 gtgttcctat tcgtatggat tcgcgagctc tcctcaagtg ttaacgccta atgtaaccac    3557
246 tcctttttaag ggagacgatg tttacttgaa tggagactgc gcttttgtca atgtctatgc   3617
247 aggagctgaa gaaggttcga ttatctcagc taatggcgac aatttaacga ttaccggaca    3677
248 aaaccataca ttatcattta cagattctca agggccagtt cttcaaaatt atgccttcat    3737
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251 agtgattttc tgggataact ccgtggggta ttctccttta tctactgtgc caacctcatc    3917
252 atcaactccg cctgctccaa cagttagtga tgctcggaaa gggtctattt tttctgtaga    3977
253 gactagtttg gagatctcag gcgtcaaaaa aggggtcatg ttcgataata atgccgggaa    4037
254 tttcggaaca gtttttcgag gtaagaataa taataatgct ggtggtggag gcagtgggtt    4097
257 ccgctacacc atcaagtacg acttttacag ttaaaaactg taaagggaaa gtttcttttca   4157
258 cagataacgt agcctcttgc ggaggcggag tggtttataa aggcattgtg cttttcaaag    4217
259 acaatgaagg aggcatattc ttccgaggga acacagcata cgatgattta aggattcttg    4277
260 ctgctactaa tcaggatcag aatacggaga caggaggcgg tggaggagtt atttgctctc    4337
261 cagatgattc tgtaaagttt gaaggcaata aaggttctat tgttttttgat tacaactttg   4397
262 caaaaggcag aggcggaagc atcctaacga aagaattc                            4435
264 <210> SEQ ID NO: 2
265 <211> LENGTH: 1012
266 <212> TYPE: PRT
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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 08/07/2002
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L:429 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:469 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:495 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
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